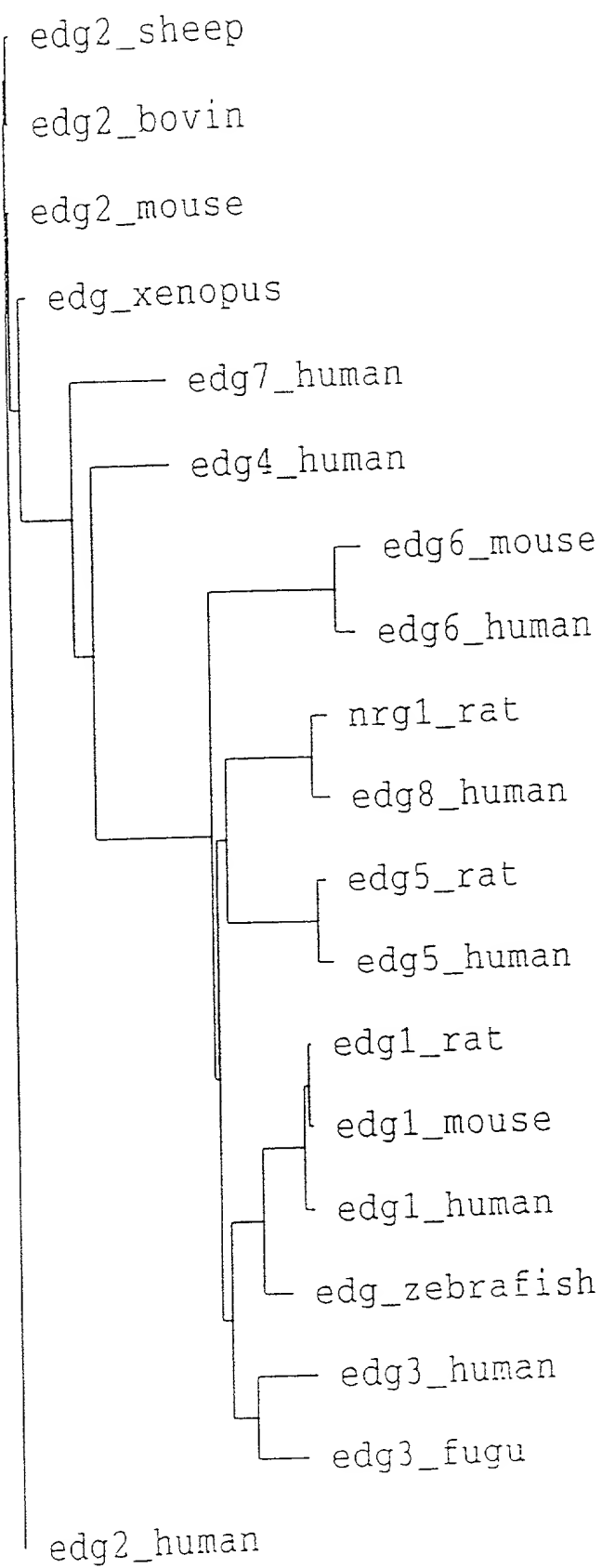


FIG 1A

1 ATGGAGTCGGGGCTGCTGCGGCCGGCGCCGGTGAGCGAGGTCATCGTCCTGCATTACAAC
 M E S G L L R P A P V S E V I V L H Y N
 61 TACACCGCAAGCTCCGCGGTGCGCGCTACCAGCCGGGTGCCGGCCTGCGCGCCGACGCC
 Y T G K L R G A R Y Q P G A G L R A D A
 121 GTGGTGTGCCTGGCGGTGTGCGCCTTCATCGTGCTAGAGAATCTAGCCGTGTTGTTGGTG
 V V C L A V C A F I V L E N L A V L L V
 181 CTCGGACGCCACCCGCGCTTCCACGCTCCCATGTTCTGCTCCTGGGCAGCCTCACGTTG
 L G R H P R F H A P M F L L L G S L T L
 241 TCGGATCTGCTGGCAGGCGCCGCTACGCCGCAACATCCTACTGTGCGGGCCGCTCACG
 S D L L A G A A Y A A N I L L S G P L T
 301 CTGAAACTGTCCCCCGCGCTCTGGTTCGCACGGGAGGGAGGCGTCTTCGTGGCACTCACT
 L K L S P A L W F A R E G G V F V A L T
 361 GCGTCCGTGCTGAGCCTCCTGGCCATCGCGCTGGAGCGCAGCCTCACCATGGCGCGCAGG
 A S V L S L L A I A L E R S L T M A R R
 421 GGGCCCGCGCCCGTCTCCAGTCGGGGGCGCACGCTGGCGATGGCAGCCGCGGCCTGGGGC
 G P A P V S S R G R T L A M A A A A W G
 481 GTGTCGCTGCTCCTCGGGCTCCTGCCAGCGCTGGGCTGGAATTGCCTGGGTGCGCTGGAC
 V S L L L G L L P A L G W N C L G R L D
 541 GCTTGCTCCACTGTCTTGCCGCTCTACGCCAAGGCCTACGTGCTCTTCTGCGTGCTCGCC
 A C S T V L P L Y A K A Y V L F C V L A
 601 TTCGTGGGCATCCTGGCCGCTATCTGTGCACTCTACGCGCGCATCTACTGCCAGGTACGC
 F V G I L A A I C A L Y A R I Y C Q V R
 661 GCCAACGCGCGCGCCTGCCGGCACGGCCCGGGACTGCGGGGACCACCTCGACCCGGGGC
 A N A R R L P A R P G T A G T T S T R A
 721 CGTCGCAAGCCGCGCTCGCTGGCCTTGCTGCGCACGCTCAGCGTGGTGCTCCTGGCCTTT
 R R K P R S L A L L R T L S V V L L A F
 781 GTGGCATGTTGGGGCCCCCTCTTCCTGCTGCTGTTGCTCGACGTGGCGTGCCCGGCGCGC
 V A C W G P L F L L L L L D V A C P A R
 841 ACCTGTCCTGTACTCCTGCAGCCCGATCCCTTCCTGGGACTGGCCATGGCCAACCTCACTT
 T C P V L L Q A D P F L G L A M A N S L
 901 CTGAACCCCATCATCTACACGCTCACCAACCGCGACCTGCGCCACGCGCTCCTGCGCCTG
 L N P I I Y T L T N R D L R H A L L R L
 961 GTCTGCTGCGGACGCCACTCCTGCGGCAGAGACCCGAGTGGCTCCCAGCAGTCGGCGAGC
 V C C G R H S C G R D P S G S Q Q S A S
 1021 GCGGCTGAGGCTTCCGGGGGCTGCGCCGCTGCCTGCCCCGGGCTTGATGGGAGCTTC
 A A E A S G G L R R C L P P G L D G S F
 1081 AGCGGCTCGGAGCGCTCATCGCCCCAGCGCGACGGGCTGGACACCAGCGGCTCCACAGGC
 S G S E R S S P Q R D G L D T S G S T G
 1141 AGCCCCGGTGACCCACAGCCCGCCGACTCTGGTATCAGAACCGGCTGCAGACTGA
 S P G A P T A A R T L V S E P A A D *



```

1
edg2_human MAAISTSIPIV ISQPQFTAMN EPQCFYNESI AFFYNRSRKH LAT.EWNTVS KLVNGL..GI
edg7_human -----MNIE..CHYDKHM DEFFYNRSNTD TVD.DW.TGT KLVIVLCVGT
edg4_human -----MVI MGQCYNETI GFFYNMSGKE LSS.HWR..P KDVTVVALGL
edg1_human -----MGPTS VPLVKAHRSS VSDYVNYDII VRHYNYTGKL ..NISADKEN SIKLTSVVFPI
edg3_human -----MATALP9R LQPVRGNETL REHYQYVGKL AGRLEASEG S.TLTTVLFL
edg5_human -----MGSL YSEYLNPNKV QEHYNYTKE. ..TLETQETT SRQYASAFIV
edg8_human -----MESGL LR2APVSEVI VLHYNYTGKL RG.ARYQPGA GLR2APVCL
edg6_human -----MNATG TPVAPESCQQ LAAGGHSRLI VLHYNHSRGL AGR.GGPEDG GLGALRGLSV

```

```

51
edg2_human TVCIFIIMLAN LLVMVAIYVN RRFHEPIYYL MANLAAADFF AGLAYFYLMF NTGPNTRRLT
edg7_human EFCLEIFFSN SLVIAAVIKN RRFHEPIYYL LANLAAADFF AGIAYVFLMF NTGPVSKTLT
edg4_human TVSVLVLLTN LLVIAAIA5N RRFHQPIYYL LGNLAAADLF AGVAYVFLMF NTGPRTARLS
edg1_human LICCFIILEN IFVLLTIWKT KKFHPPIYYF IGNLALSOLL AGVAYTANLL LSGATTYKLT
edg3_human VICSFIVLEN LMVLIAMKN NKFHNRMYYF IGNLALCOLL AGIAYKVNIL MSGKKTFSLS
edg5_human ILCCAIVVEN LLVLIAVARN SKFHSAMYLF LGNLAASOLL AGVAFVANTL LSGSVTLRLT
edg8_human AVCAFIIVLEN LAVLLVLGRH PRFHPMFLL LGSLTLSOLL AGAAYAANIL LSGPLTLKLS
edg6_human AASCLVULEN LLVLAATSH MRSRPWVYYC LVNITLSOLL TGAAYLANVL LSGARTFRLA

```

```

121
edg2_human VSTWLLRCGL IDTSLTASVA NLLAIAIERH ITVER.MQLH TRMSNRPRVVV VIVVIWTMAT
edg7_human VNRWFLRCGL LDSSLTASLT NLLVIAVERH MSIMR.MRVH SNLTKKFVTL LILLVWAIAI
edg4_human LEGWFLRCGL LDTSLTASVA TLLAIAVERH RSVMA.VQLH SRLPRGPRVVM LIVGVVVAAL
edg1_human PAQWFLREGS MFVALSASVF SLLAIAIERH ITMLK.MKLH NGSNNRFLFL LISACWVISI
edg3_human PTVWFLREGS MFVALGASTC SLLAIAIERH LTMIR.MRPY DANKRHRVFL LIGMCWLIAS
edg5_human PVQWFAREGS ASITLSASVF SLLAIAIERH VAIAR.VKLY GSDKSCFLL LIGASWLIISI
edg8_human PALWFAREGG VFVALTASVL SLLAIALERS LTMAR.RGPA PVSSRGRTLA MAAAANGVSI
edg6_human PAQWFLREGS LFTALAASF SLLFTAGIRF ATMVRPVAES GATKTSRVYG FIGLCWLLAN

```

```

181
edg2_human VMGAIPSVGW NCICDIENCS NMAPLYSDSY LVFWAIFNLV TFVVMVVLYA HIFGYVRQRT
edg7_human FMGAVPTLGV NCLCNISACS SLAPITYRSY LVFWTVSNLM AFLIMVVVYL RIYVYVKKRT
edg4_human GLGLLPASHW HCLCALDRCS RMAPLLRSY LAVWALSLL VLLMVAVYT RIFFYVRRRV
edg1_human ILGGLPIMGW NCISALSSCS TVLPLYKHXY ILFCTTVETL LLLSIVILYC RIYSLVTRTS
edg3_human TLGALPILGW NCLHNLPOCS TILPLYKXY IAFCSISFA ILVTIVILYA RIYFLVKSSS
edg5_human VLGGLPILGW NCLGHLEACS TVLPLYKXY VLVVTFISI ILLAIVALYV RIYCVVRSSH
edg8_human LLGLLPALGW NCLGRLDACS TVLPLYKXY VLFVCLAFVG ILAICALYA RIYCVVRANA
edg6_human LLGMLPILGW NCLCAFDRCS SLLPLYKXY ILFCLVIFAG VLATIMGLYG AIFRLVQASG

```

```

241
edg2_human MRMSRHSSGP R.....RNR DTMSLLKTV VIVLGAFTIC WTPGLVLLLL D.VCCP..QC
edg7_human NVLSPHTSGS I.....SRR RTPMKLMKTV MTVLGAFVVC WTPGLVLLLL DGLNCR..QC
edg4_human QRMAEHVSCH P.....RYR ETTL5LVKT VIVLGAFVVC WTPGQVLLLL DGLGCE..SC
edg1_human RRLTFR.... .KNISKASRS SENVALLKT VIVLGVFIAC WAPLFTLLLL DV.GCKVKRT
edg3_human RKVANH.... .NN.....S ERSALLRTV VIVVSVFIAC WSPLFIFLFI DV.ACRVQAC
edg5_human ADMA..... .A PQTALLKTV TIVLGVFIVC WLPAFSILL DV.ACPVHSC
edg8_human RRLPARPGTA GTTSTRARRK PRSLALLRT SVVLLAFVAC WGPLFLLLL DV.ACPARTC
edg6_human QKAP..... .RPAARRK ARR...LLKTV LMILLAFVVC WGPLFGLLLA DVFSGNLWQA

```

```

301
edg2_human DVLAYEYFFL LLAEFNSAMN PIISYRKE MSATFRQILC QRSENPTGP TESSORSASS
edg7_human GVQHVKKWFL LLALLNSVYN PIISYKDED MYGTMKMIC CFSQENP... ..ERRPSR
edg4_human NVLAVEYFFL LLAENSLVN AAVYSCRDAE MRRTFRALLC CACLRQSTRE SVHYTSSAGQ
edg1_human DILFRASYFL VLAVLNSGTN PIITYLTKE MRAFTIRMS CCKCPSGD... ..S
edg3_human PILFKAQWFI VLAVLNSAMN PVIYTLASKE MRAFFRLV. .CNC.LVR... ..G
edg5_human PIYKAYYFF AVSTLNSLLN PVIYTWRSRD LRREVLAPLQ CWRPGVGV... ..Q
edg8_human PVLLQADPFL GLAMANSLLN PIITYTLTRD LRHALLRLVC CGRHSCGRDP SGS..QQSAS
edg6_human SYLRGMFWIL ALAVLNSAVN PIISYRSRE VCRVLSFLC CGLRLGMRG PGDCLARAVE

```

```

361
edg2_human LNHTILAGVH SNOHSVV--- -----
edg7_human IPSTVLSRSD TGSQYIEDSI SQGAVCNKST S-----
edg4_human GASTRIMLPE NGHPLMTPE SYLELQRYAA SNKSTA200L WVLLAQPNQC D-----
edg1_human AGKFRPIIA GMEFSRSK.. .SONSSHPOK DECONPETIM SSGNVNSSS- -----
edg3_human RGARASPIQP ALOPSRSKSS SSNNSSHSPK VKEDLPHTOP SSCIMOKNAA LQNGIFCN
edg5_human GRRRVGTPEH HLLPLRSSSS LERGMHMPST PTFLEGNTVV -----
edg8_human AAEASGGLRR CLPPGLOGSF SGSESSPQR OGLDTSGETG SPGAPTAART LVSEPAAD
edg6_human AHSAGSTDS SLRP.ROSER GSRSLFRMR EPLSSISSYR SI-----

```

Fig. 1C

FIG 2A

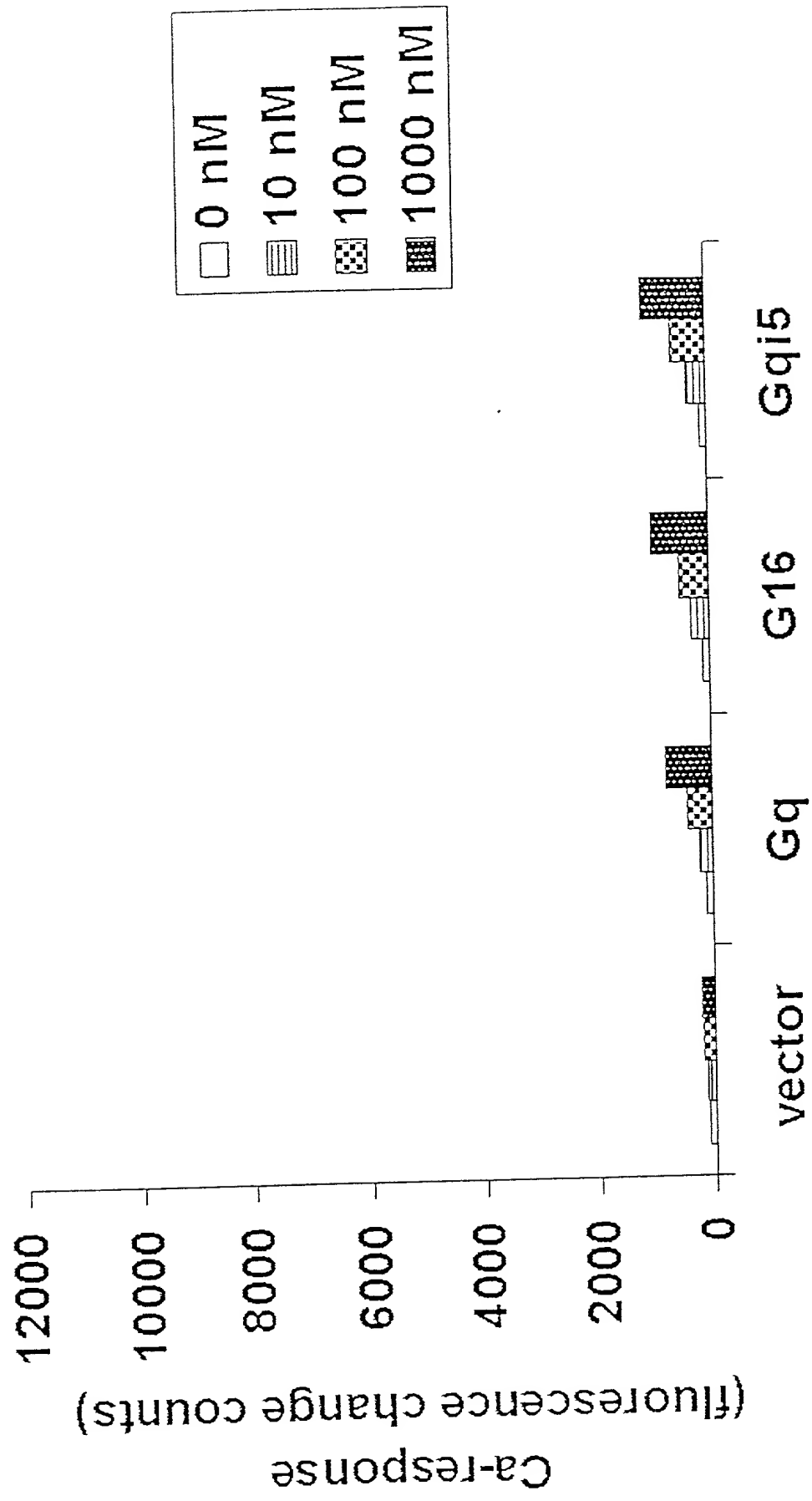


FIG 2A: 9464360

4/22

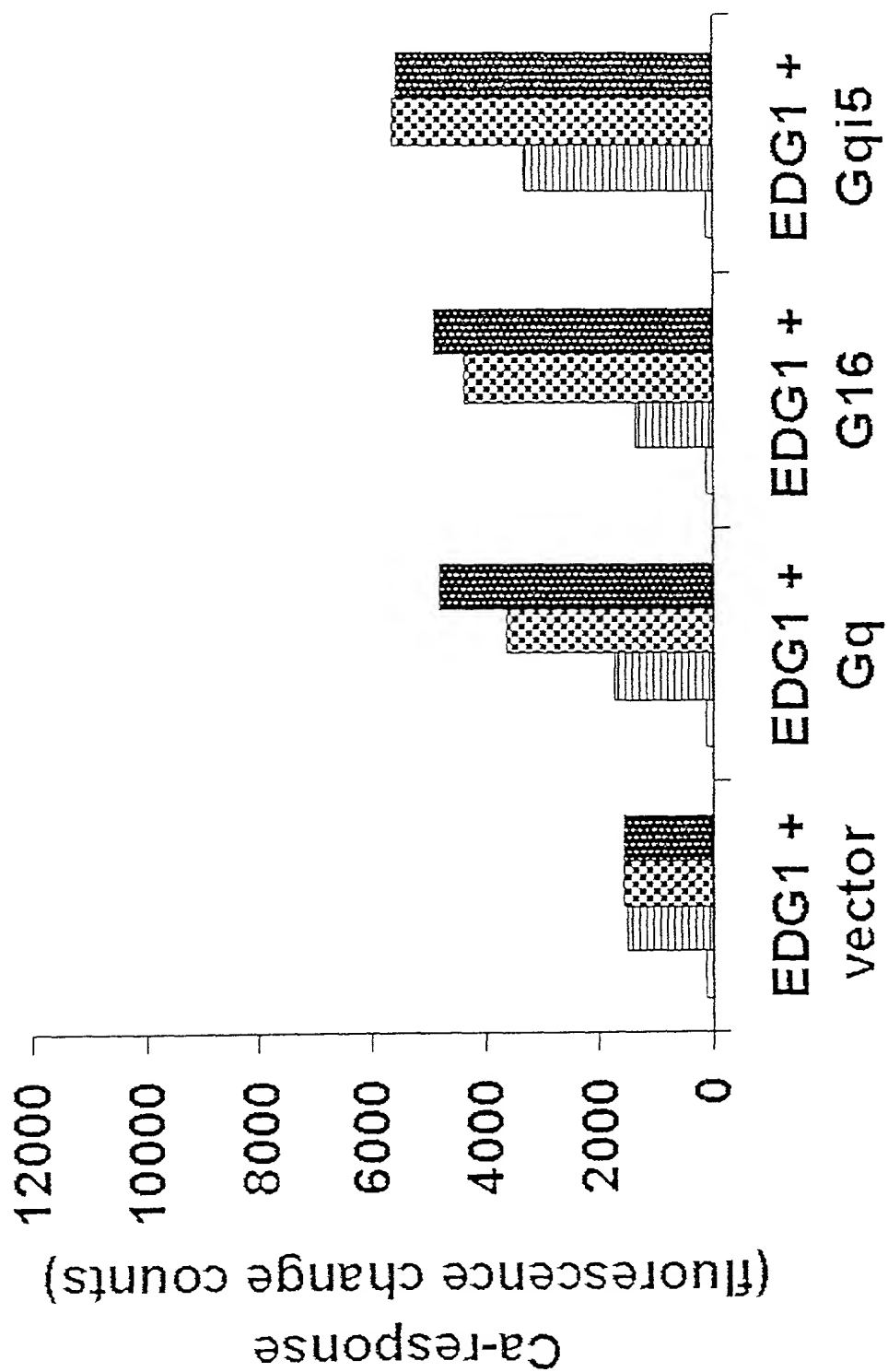
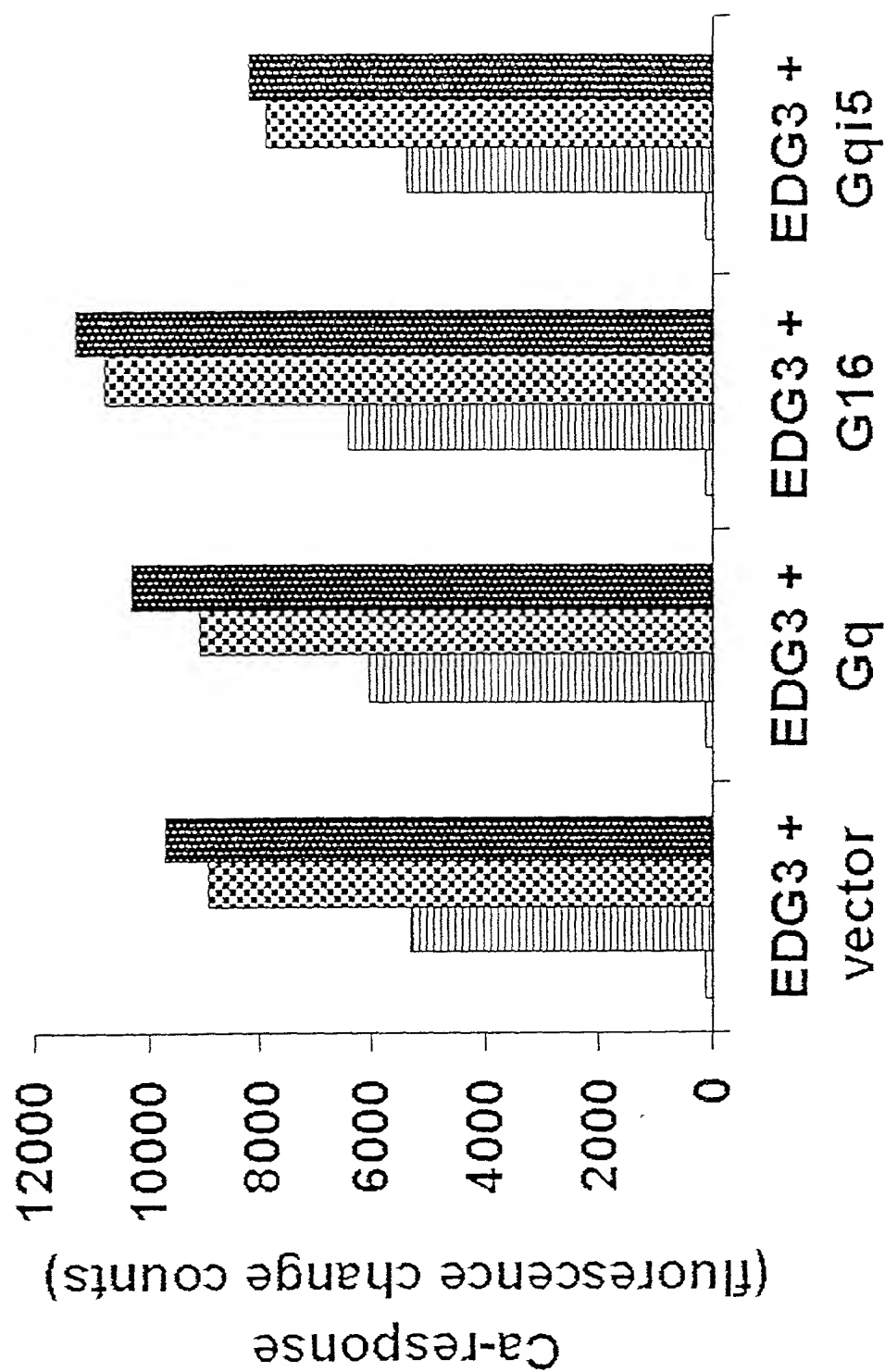


FIG 2C

6/22



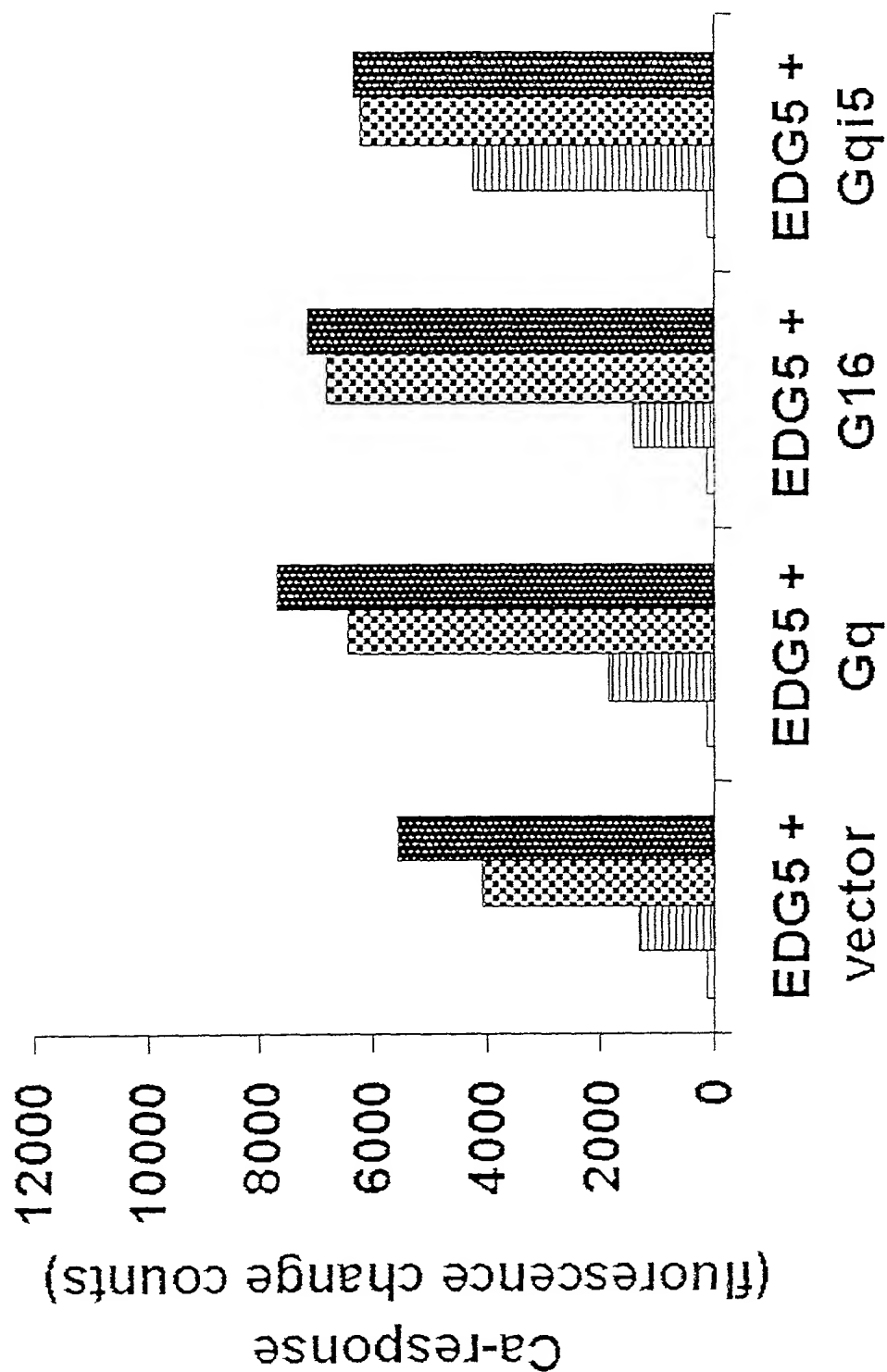


FIG 2D 9/27/00

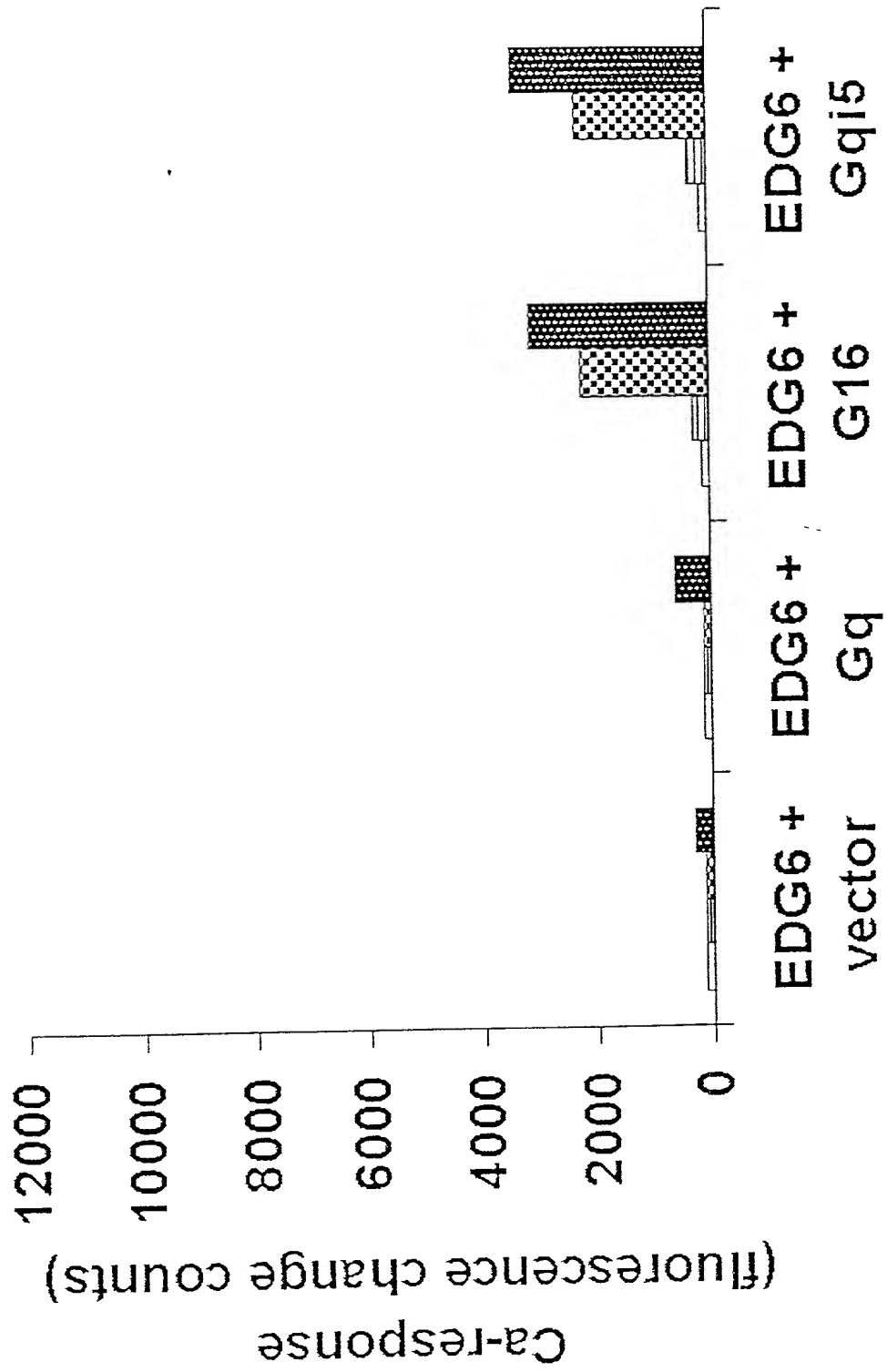


FIG 2F

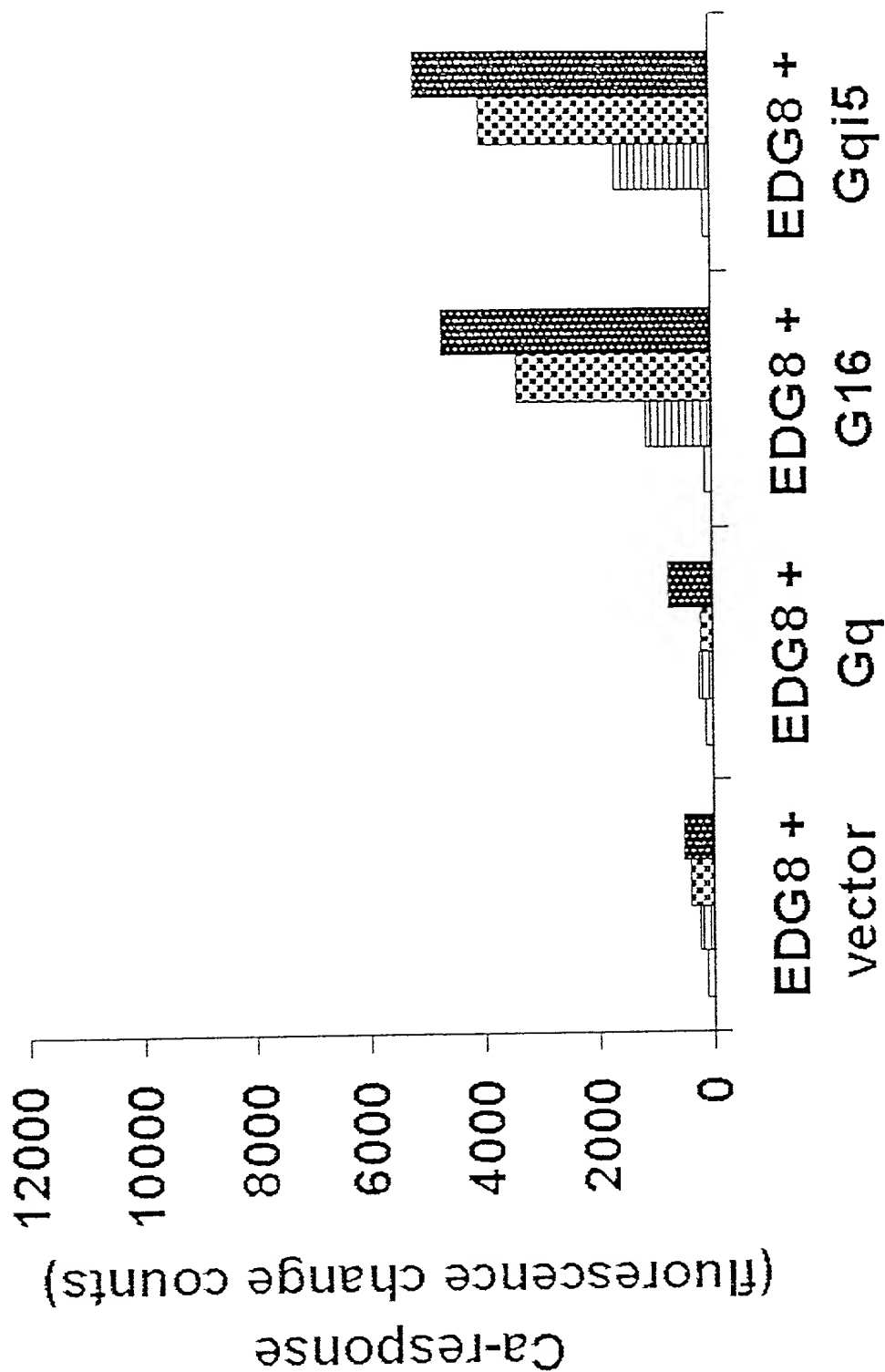


FIG 3

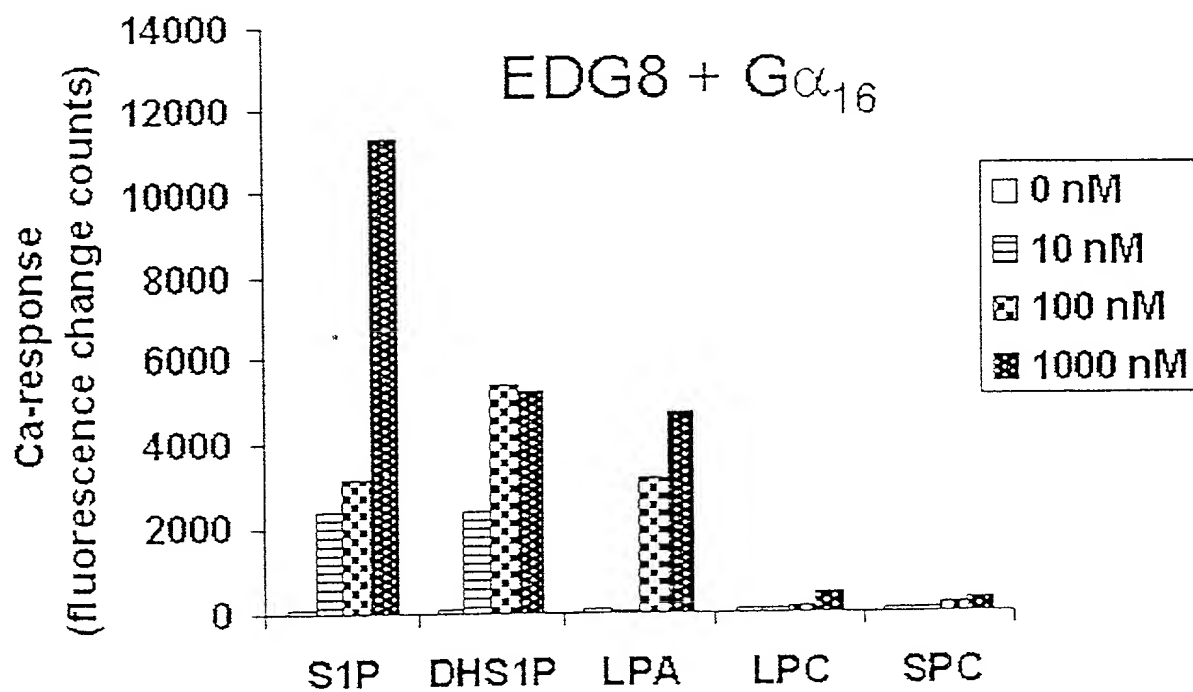
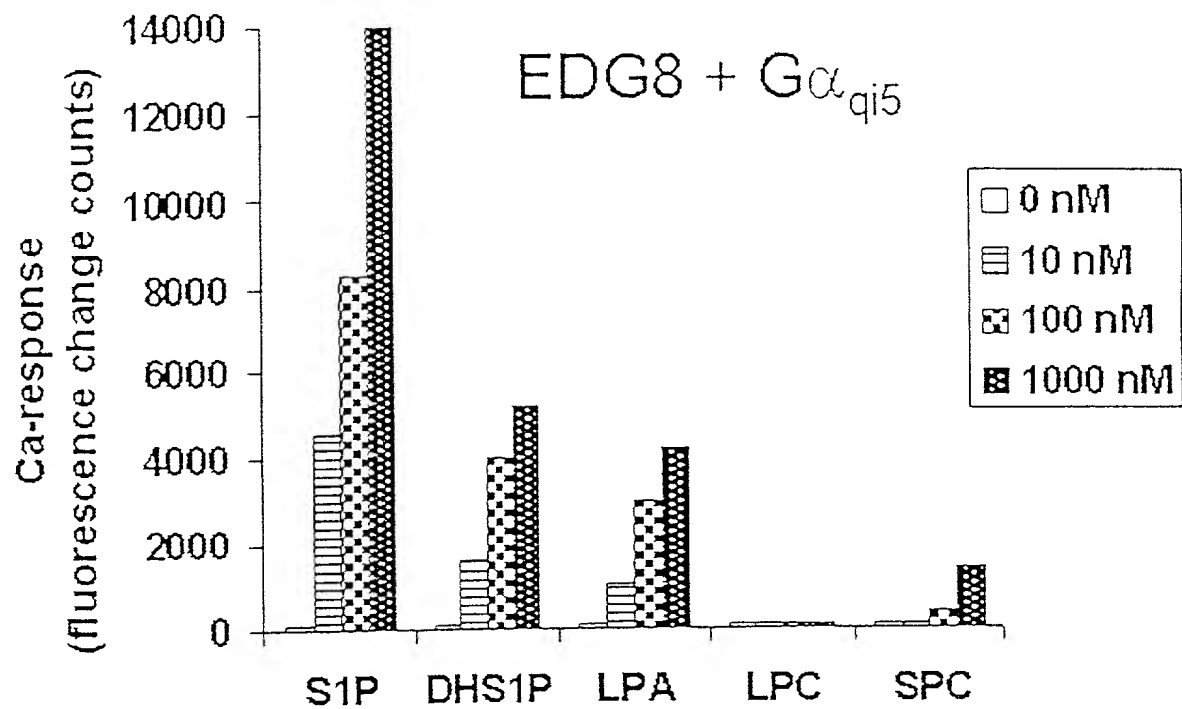


FIG 4

Human EDG8 tissue expression

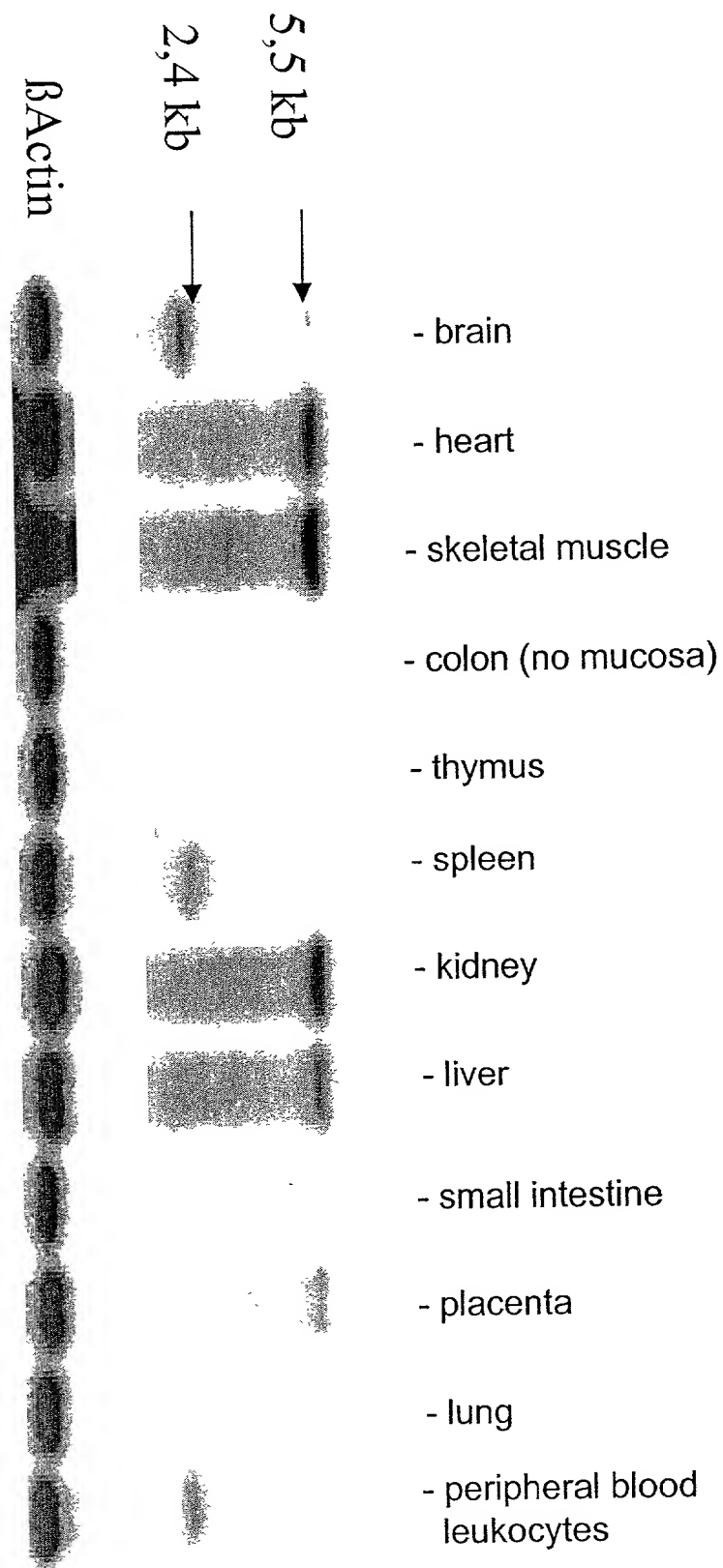
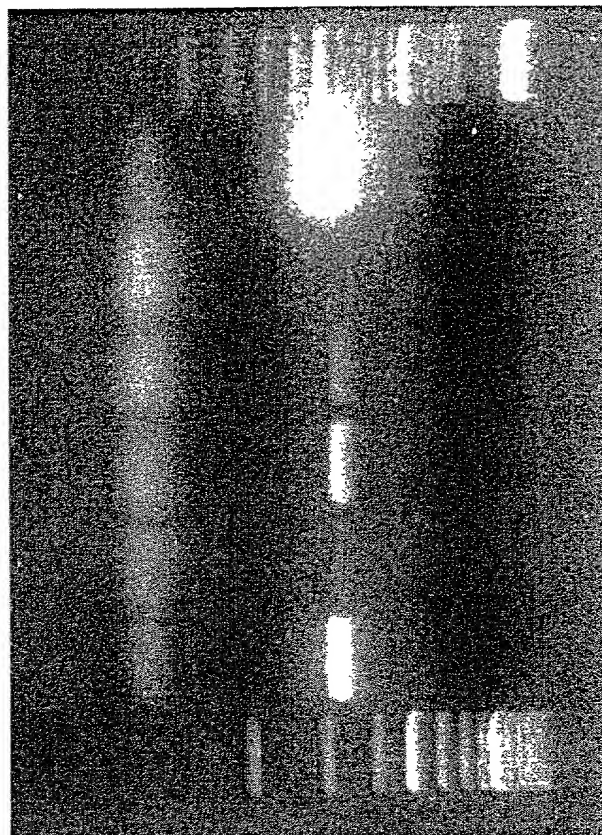
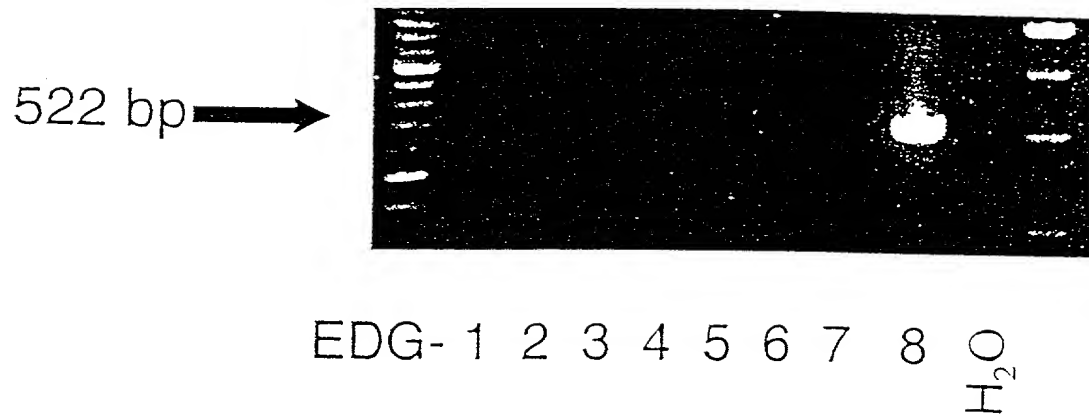


FIG 5A

522 bp
↓

Pos. control
neg. control
HUVECS
HCAEC
HMVEC-L
HPAEC

FIG 5B



qi5 background

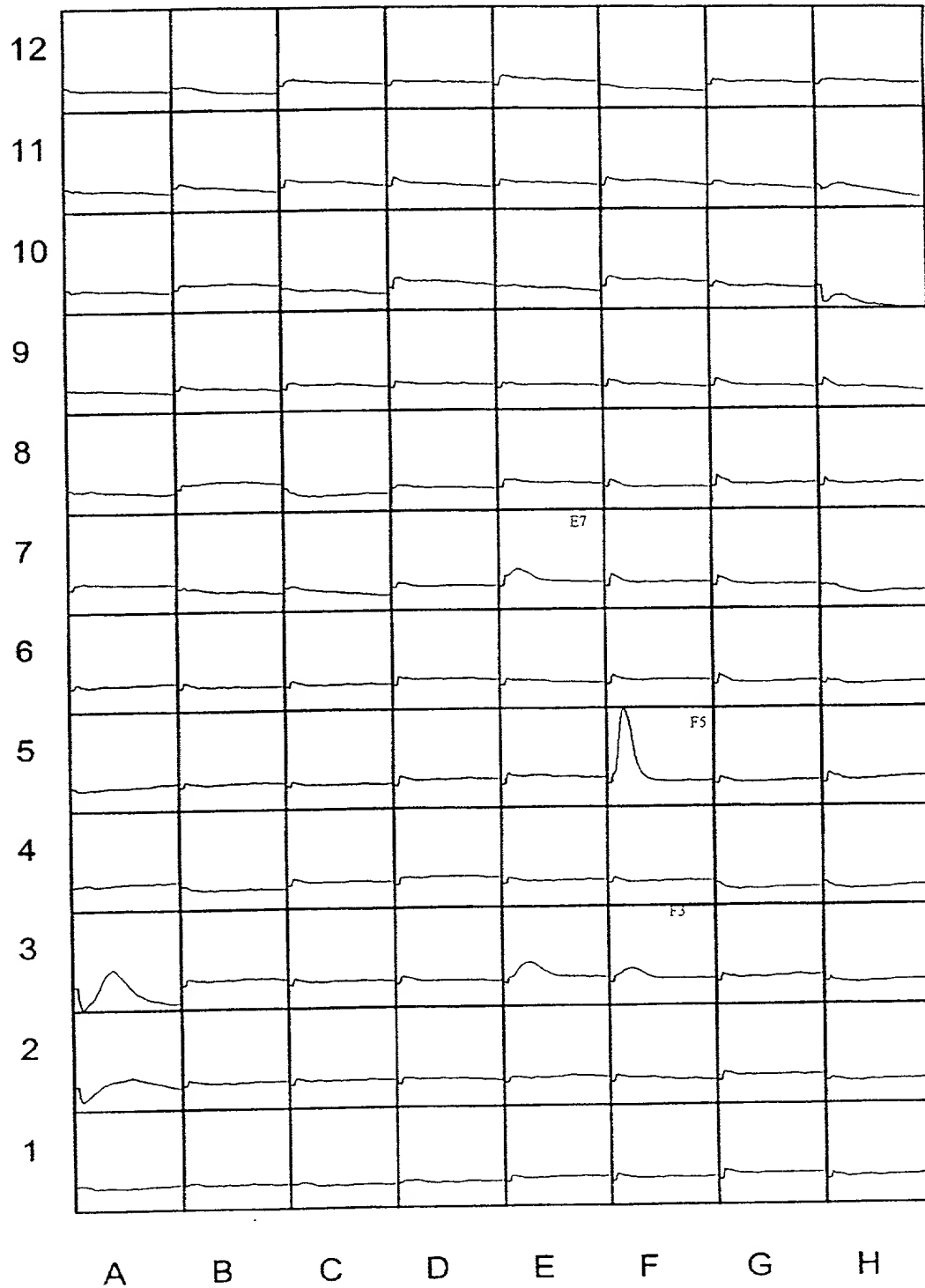


Fig. 6B

rEDG8

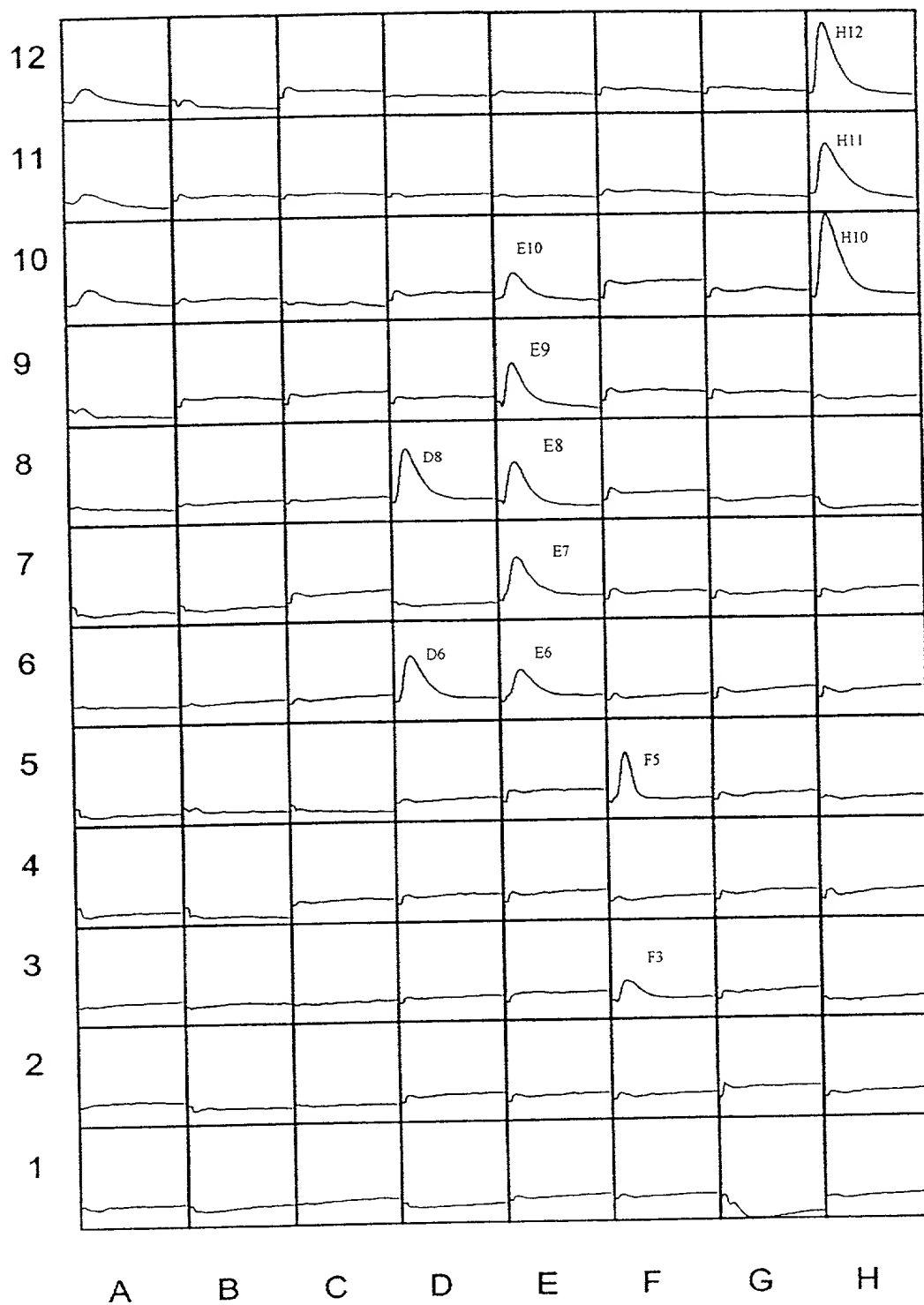


Fig.6C

Fluorescence Change counts

Wells	Lipid	background	rEDG8	stand. response
H10-H12	1 μ M S1P	0	5196	5196
F5	1 μ M LPA	5893	4327	-1566
F3	1 μ M cPAF	1017	1570	553
E10	1 μ M EPA PAF	0	1354	1354
E9	1 μ M AA PAF	0	3121	3121
E8	1 μ M Enantio PAF	0	3883	3883
E7	1 μ M paf C18:1	1256	3765	2509
E6	1 μ M Lyso PAF	0	2421	2421
D8	1 μ M dhS1P	0	5144	5144
D6	1 μ M S1P	0	3672	3672

Fig. 7A

qi5 background in HEK

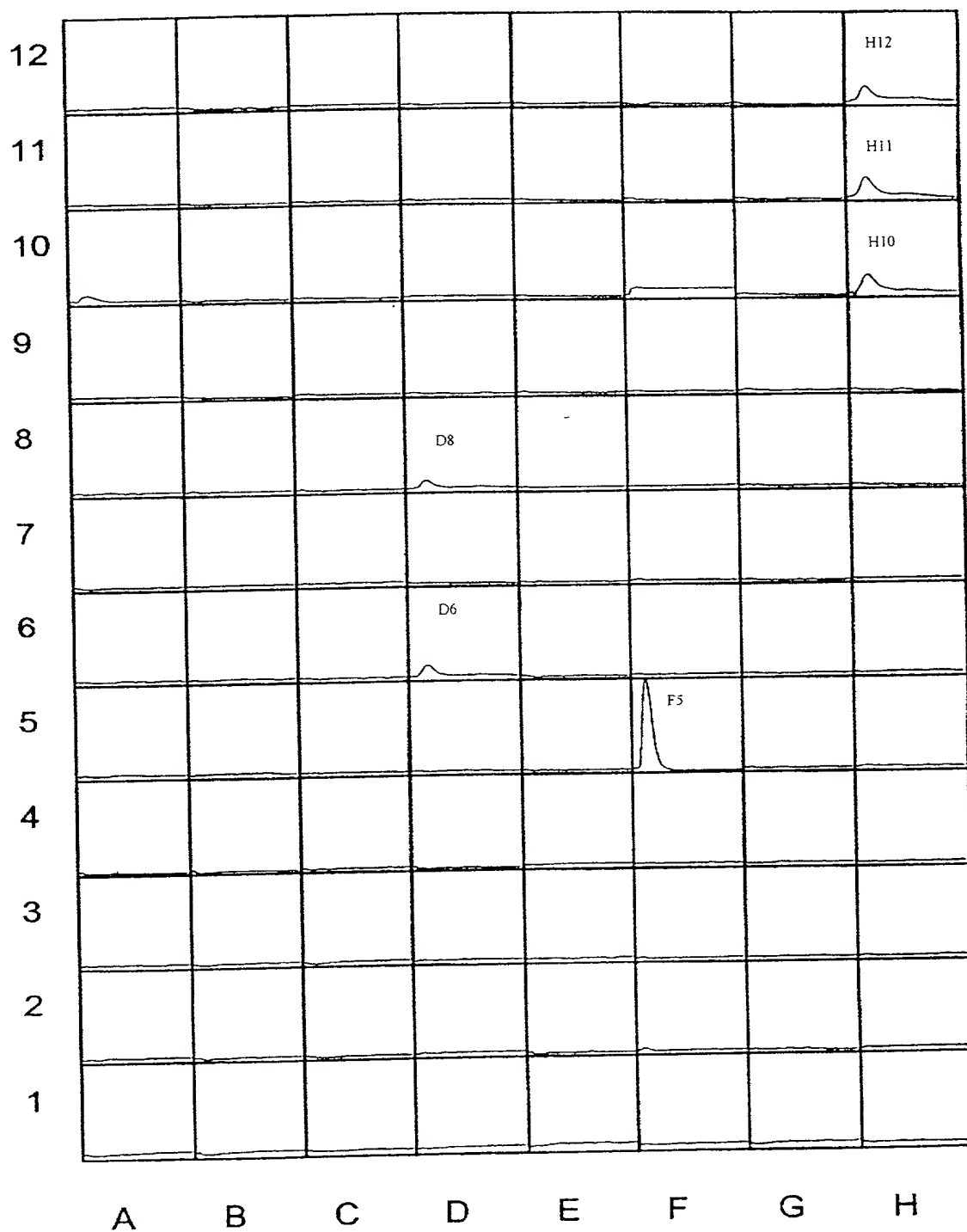
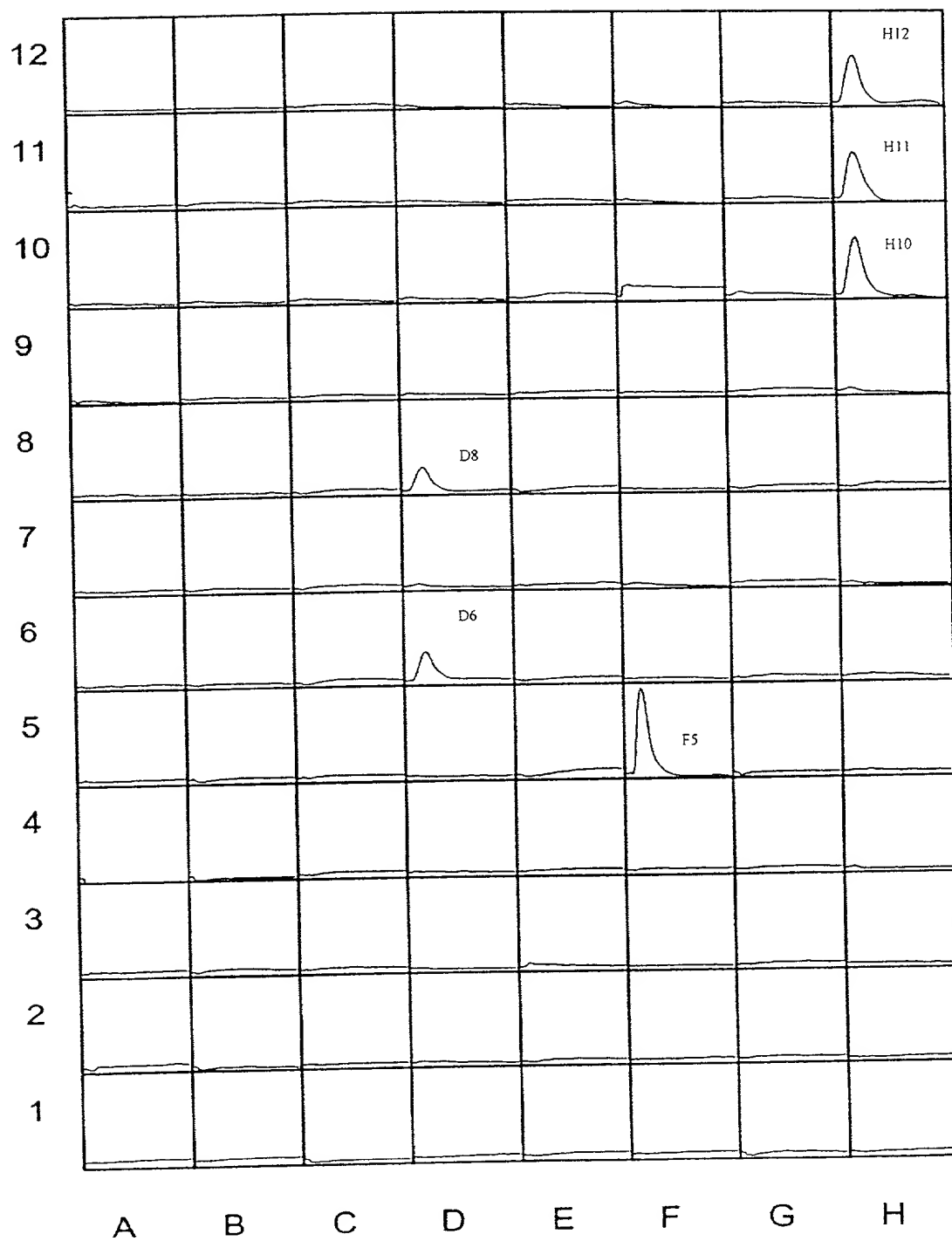


Fig. 7B

hEDG8



Fluorescence change counts

Wells	Lipid	background	hEDG8	stand. response
H10-H12	1μM S1P	3696	9493	5797
F5	1μM LPA	18004	16333	-1671
D8	1μM dhS1P	1683	4522	2839
D6	1μM S1P	2273	5605	3332

Fig. 7C

FIG 8

% S1P response

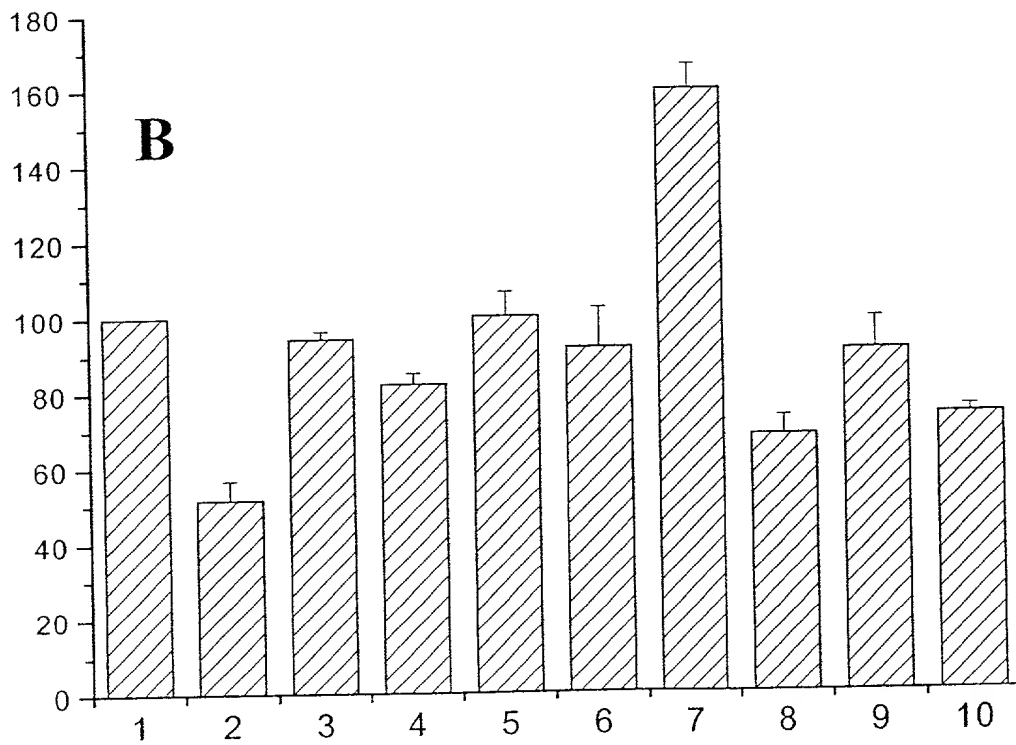
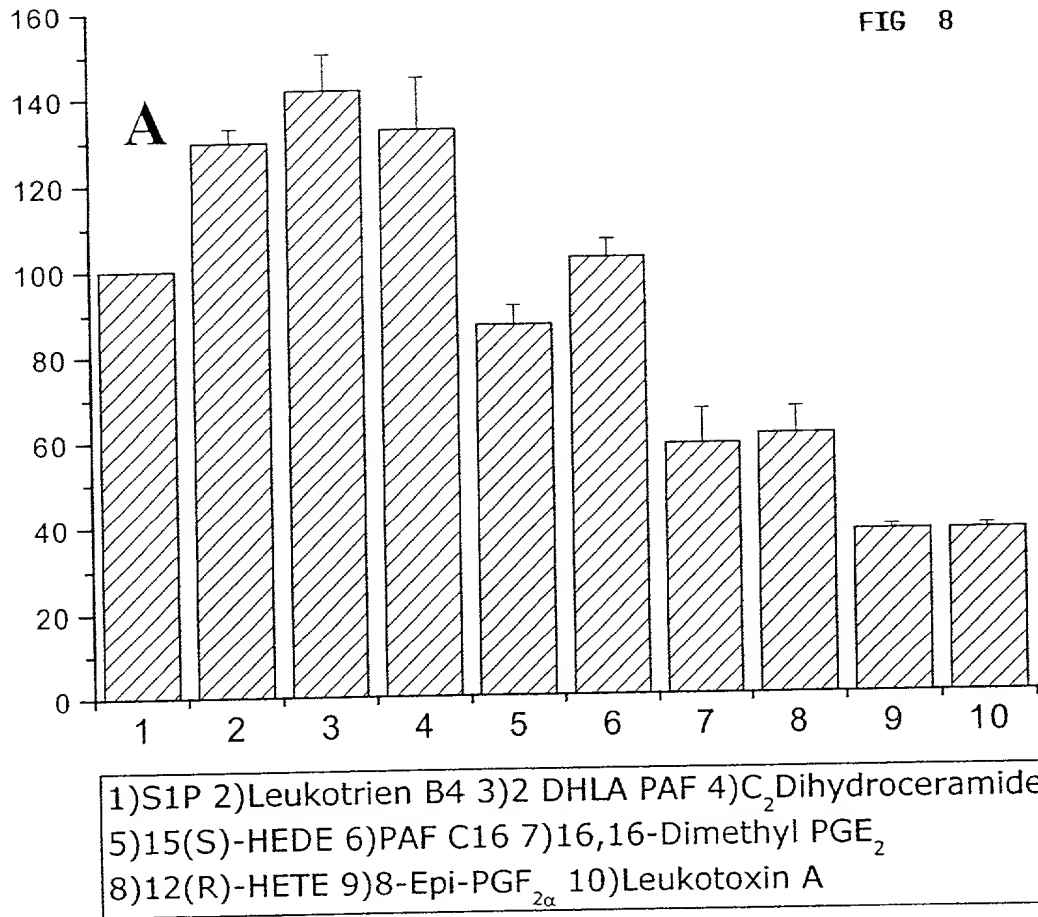
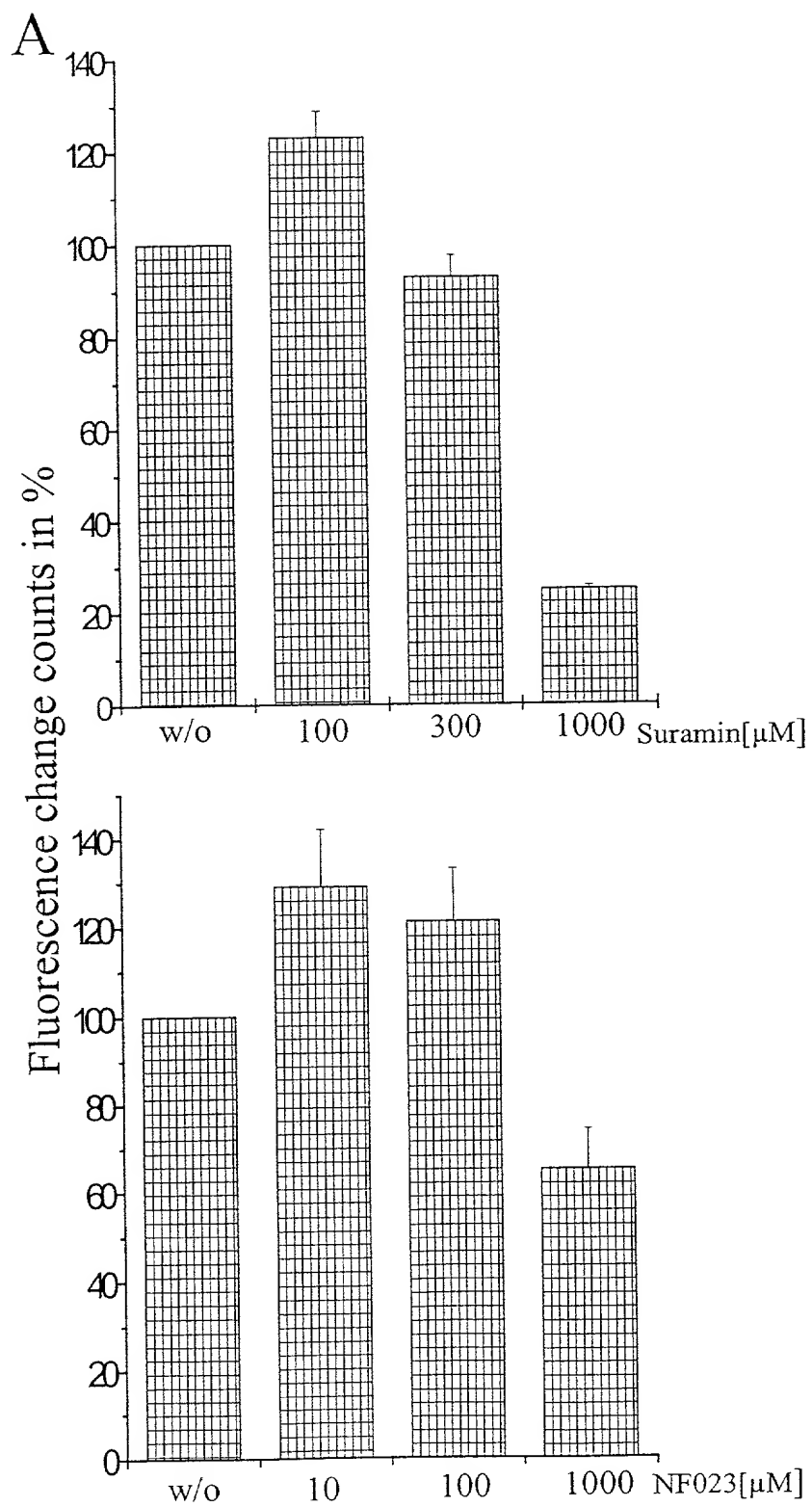


FIG 9A



FTG 9B

